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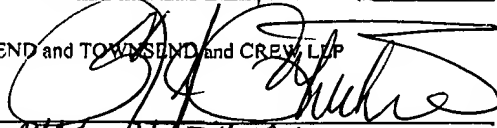
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On

MARCH 5, 2004

TOWNSEND and TOWNSEND and CREW, LLP

By:


STEPHANIE WHITEHURST

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

Lemaux, *et al.*

Application No.: 09/384,811

Filed: August 27, 1999

For: TRANSPOSON TAGGING AND
GENE DELIVERY IN SMALL GRAIN
CEREALS

Examiner: Cynthia Collins

Art Unit: 1638

DECLARATION UNDER 37 C.F.R. §1.132
BY PEGGY LEMAUX, Ph.D.

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

1. I, Peggy Lemaux, Ph.D., am a Cooperative Extension Specialist at the University of California, Berkeley and am currently the Director of the University of California Division of Agriculture and Natural Resources Biotechnology Workgroup. I am a co-inventor of the subject matter of the above-referenced patent application. I have worked in the field of plant genetics for over 15 years.

2. I hold a Ph.D. from the University of Michigan, which was conferred in 1977. I have authored over 65 publications relating to microbial and plant genetics and molecular biology. A copy of my curriculum vitae is attached as Exhibit 1.

3. I have read and am familiar with the contents of the above-referenced patent application and claimed subject matter. It is my understanding that the Examiner has rejected the claims as allegedly unpatentable over the prior art.

4. This declaration is provided to show that prior art gene delivery methods have been plagued by problems of gene inactivation. As explained below, transposase-mediated gene delivery in barley is surprisingly effective in producing transgenic barley plants with stable transgene expression through generation advance. In particular, as compared to prior art methods, such as biolistics, electroporation and *Agrobacterium*-mediated gene delivery, methods of the present invention result in a greater percentage of single copy insertions, and they are much less prone to gene silencing. In addition, unlike prior art methods, transposons preferentially insert in transcriptionally active regions of the barley genome (more than 80% of the time), which further limits the degree of transgene silencing.

5. The attached publication by my colleagues and me [Koprek *et al.*, *Plant Physiol.* 125:1354-1362 (2001), Exhibit A] describes experiments in which we analyzed barley plants made by the methods claimed in the present application. At the time we made our invention, gene inactivation had been observed in many transgenic plants and was especially problematic in cereals. Biolistics, the most commonly used method of transformation, leads to complex, multicopy transgene integration that results in gene silencing in more than 50% of transgenic plants (*see*, Koprek *et al.* page 1354, first column). Since the successful use of transgenic plants in agriculture requires the development of plants that stably express the transgene during generation advance, there is much interest in developing methods that overcome these problems. As of the time Koprek *et al.* was published, as well as the filing of the present application, these problems had not yet been solved.

6. The presently claimed methods, however, provide a surprisingly effective means for achieving these goals. The methods of the invention comprise introducing into a barley plant an element containing a desired expression cassette bordered by approximately 250 base pair of *Ds* inverted repeat DNA on the 5' and 3' ends. The *Ds* element carrying the transgene can be activated to move throughout the plant genome through transposase-mediated excision and reintegration. Barley plants are then selected

in which the *Ds* element has reinserted. As demonstrated in Koprek *et al.*, the methods of the invention provide an unusually high percentage of transformants with single copy insertions and that that avoid the problems of gene silencing and thus lead to stable transgene expression through generation advance (*see*, page 1355, first column).

7. As explained on page 1360 of Koprek *et al.*, a *Ds* element carrying a selectable marker gene (*bar* which confers resistance to the herbicide Basta) was introduced into plants by particle bombardment. These plants were then crossed with *Ac* transposase expressing plants. Resulting F_1 plants were selfed and F_2 plants were analyzed to identify plants in which the *Ds* element had transposed and segregated away from the *Ac* transposase gene. These plants are referred to in the paper as "TNP" plants. Plants which lack an expressing transposase gene and in which the *Ds* transposon is thus at the original site of integration are referred to as "nTNP" plants.

8. Table 1 on page 1356 shows the results of the analysis of single copy TNP and single and multiple copy nTNP plants for stable transgene expression through the F_4 generation. There it can be seen that only 6 of 35 (17%) F_3 generation TNP lines had gene silencing, as measured by sensitivity to Basta, whereas transgene expression in 14 of 17 (82%) F_3 generation nTNP lines was silenced. In the F_4 generation, 7 of 35 (20%) of TNP lines showed gene silencing, compared to 16 of 17 (94%) in nTNP lines. Thus, in the F_4 generation, 80% of TNP lines expressed the transgene, as opposed to only 6 % in the nTNP lines.

9. Comparing only barley plants comprising a single copy of the transgene showed even more stability in TNP plants relative to nTNP plants. Table 1 of Koprek *et al.* shows that lines derived from F_1 plants A8-1 and A8-5 (both of which have a single *Ds* element) had 84% of TNP lines expressing the transgene in both the F_3 and F_4 generations (gene silencing in 4 of 25 or 16%).

10. These results are also illustrated in Figure 2, which shows the large difference in transgene expression (TGE) instability in TNP plants through the F_4 generation, as compared to single and multiple copy nTNP plants. Thus, these experiments show that transposase-mediated excision and reinsertion dramatically increases the stability of transgene expression in barley from genes located between the

Ds inverted repeat sequences and which transpose to transcriptionally active regions of the genome.

11. We also investigated the unusual stability of the gene expression in TNP plants by analyzing the integration sites of the transposed *Ds* elements. As shown in Figure 3 and discussed in the second column of page 1356, the *Ds* elements in these plants had integrated in single to low copy regions of the genome (*i.e.*, transcriptionally active regions of the genome). As we noted at page 1359, second column, a factor that may play a decisive role in the unusual stability of the transgenes in these plants is that approximately 80% of the *Ds* elements re-inserted into single to low copy genomic regions.

12. We conclude our paper by stating that the use of transposable elements in gene delivery "leads to large numbers of independent single-copy transgenic plants." In addition, the increased stability in TNP plants "gives rise to a system of gene delivery that has great utility for generating crop plants with improved agronomic characteristics." (page 1360, first column). We could make such a statement only if the reviewers of the manuscript in this prestigious journal were also convinced that this is true.

13. I further declare that all statements made herein of my knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements are made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment or both (18 U.S.C. § 1001), and may jeopardize the validity of the patent application or any patent issuing thereon.

Date: March 5, 2004

By: 

Peggy Lemaux, Ph.D.

Transposon-Mediated Single-Copy Gene Delivery Leads to Increased Transgene Expression Stability in Barley¹

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Instability of transgene expression in plants is often associated with complex multicopy patterns of transgene integration at the same locus, as well as position effects due to random integration. Based on maize transposable elements *Activator* (*Ac*) and *Dissociation* (*Ds*), we developed a method to generate large numbers of transgenic barley (*Hordeum vulgare* var Golden Promise) plants, each carrying a single transgene copy at different locations. Plants expressing *Ac* transposase (*AcTPase*) were crossed with plants containing one or more copies of *bar*, a selectable herbicide (Basta) resistance gene, located between inverted-repeat *Ds* ends (*Ds-bar*). F₁ plants were self-pollinated and the F₂ generation was analyzed to identify plants segregating for transposed *Ds-bar* elements. Of *Ds-bar* transpositions, 25% were in unlinked sites that segregated from vector sequences, other *Ds-bar* copies, and the *AcTPase* gene, resulting in numerous single-copy *Ds-bar* plants carrying the transgene at different locations. Transgene expression in F₂ plants with transposed *Ds-bar* was 100% stable, whereas only 23% of F₂ plants carrying *Ds-bar* at the original site expressed the transgene product stably. In F₃ and F₄ populations, transgene expression in 81.5% of plants from progeny of F₂ plants with single-copy, transposed *Ds-bar* remained completely stable. Analysis of the integration site in single-copy plants showed that transposed *Ds-bar* inserted into single- or low-copy regions of the genome, whereas silenced *Ds-bar* elements at their original location were inserted into redundant or highly repetitive genomic regions. Methylation of the non-transposed transgene and its promoter, as well as a higher condensation of the chromatin around the original integration site, was associated with plants exhibiting transgene silencing.

The successful introduction of transgenic crops into modern farming practices depends on maintaining and improving the agricultural performance of the modified plants and on the stable and predictable transmission and expression of the transgene in successive generations during seed production and commercial cultivation (McElroy, 1999). Inactivation of transgene expression has often been observed in plants and seems to be especially problematic in cereal crops. In these crop species the most frequently used biolistic transformation methods typically result in complex, multicopy transgene integration patterns, where it has been observed that more than 50% of T₁ plants exhibit transgene silencing (Wan and Lemaux, 1994; Pawlowski et al., 1998; for

review, see Iyer et al., 2000). Inactivation of expression in plants with single copies of the transgene can occur (Meyer and Heidmann, 1994), but it is not as frequent as the silencing observed when multiple copies of the transgene exist.

In addition to effects of copy number on transgene silencing (Assaad et al., 1993; Atkinson et al., 1998), this phenomenon is influenced by many other factors. These include the presence of inverted repeats in the complex integration patterns (Stam et al., 1997a, 1997b), the overexpression of the transgene (Que et al., 1997), the nature of the insertion site (Matzke and Matzke, 1998), the AT/CG composition of the transgene (Matzke and Matzke, 1998), and environmental factors (Meyer et al., 1992). These factors can trigger different mechanisms of transcriptional or post-transcriptional gene silencing.

Due to the exacerbated problems associated with transgene silencing, and especially silencing in multicopy insertion events, it is desirable to generate transgenic plants containing only a single copy of the transgene. With existing cereal transformation methods, however, the number of single-copy transgenic plants generated is usually low relative to the number of plants containing multicopy events. This is particularly problematic in crop species that are not readily transformed, since obtaining the large numbers of independent transformants to find the infrequent single insert is time consuming and costly. Furthermore, although it is possible with sufficient

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effort to identify a sufficient number of single-copy insertion events, this approach alone will not always overcome transgene expression instability problems. Transgene silencing has also been observed in events with single, simple-pattern transgene inserts associated with, for example, location of the insert, GC content of the region, and presence of vector DNA.

Attempts have been made to increase the number of single-copy transgenic plants. In general, *Agrobacterium*-mediated transformation leads to lower copy numbers of the transgene, and single-copy inserts in transgenic plants are observed more frequently. For some cereals, however, this method is not routine. Even though single-copy plants can be obtained more frequently in dicot and monocot (Cheng et al., 1997; Tingay et al., 1997) species, the use of *Agrobacterium*-mediated transformation does not circumvent the problem of transgene silencing (e.g. Ishida et al., 1996; Park et al., 1996). Other methods have been employed to increase the number of single-copy inserts, including the use of an Agrolistic method (Hansen and Chilton, 1996) and inhibitors of recombination (De Block et al., 1997). Another successful approach has been used in wheat and utilizes the bacteriophage *cre/lox* recombination system to resolve the complex integration patterns of multiple transgenes into single-copy integration patterns (Srivastava et al., 1999). However, these approaches do not always overcome transgene expression stability problems.

We developed a system in barley (*Hordeum vulgare* var Golden Promise) based on the maize transposons *Activator* (*Ac*) and *Dissociation* (*Ds*). In this system the transgene is inserted between the nonautonomous *Ds*-element inverted repeats and is translocated to different loci in the genome as a result of the action of *Ac* transposase (*AcTPase*). The *Ds* cassette carries *bar* (*Ds-bar*), which encodes phosphinothricin acetyl transferase, which confers resistance to the herbicide, Basta. This cassette can transpose to genetically unlinked sites, which segregate in the next generation from the remaining transgene copies, the other vector sequences, and the *AcTPase* gene. This method requires only a few original transformation events and results in high numbers of single-copy transgenic plants, each carrying a stabilized transgene at different genomic locations. Transposons are also subject to silencing (Fedoroff and Chandler, 1994), although at much reduced frequencies relative to most transgenes. Here we discuss the influence of transgene copy number and the nature of the integration site of the transposed *Ds-bar* element on transgene expression stability.

RESULTS

Single-Copy Transgenic Plants

From crosses between plants expressing functional *AcTPase* and plants from three independent transfor-

mants that contain one to six copies of *Ds-bar* we obtained numerous families of F₁ plants carrying both elements. Progeny of four self-pollinated F₁ plants were analyzed (200 F₂ plants derived from line A8-1 and 100 F₂ plants from A8-5, A1-5, and A18-5) to identify F₂ plants containing a single copy of transposed *Ds-bar* that had segregated away from the gene encoding *AcTPase* (*AcTPase*) and other copies of *Ds-bar*. These plants were designated "TNP" (transposed) in contrast to segregating plants designated "nTNP" (non-transposed) carrying *Ds-bar* at the original integration sites and also not containing *AcTPase*.

Among 200 F₂ progeny (designated a "family") from F₁ plant A8-1, which contained a single *Ds-bar* element at its original integration site after microparticle bombardment, we identified 21 plants (designated "lines") with a single *Ds-bar* element transposed to a new position, as confirmed by PCR and DNA-blot hybridization analysis. From F₁ plant A8-5, a sibling of A8-1 also carrying a single *Ds-bar* element at its original integration site, we obtained 17 F₂ TNP plants (hereafter referred to as lines). Among progeny of F₁ plants A1-5 and A18-5, which have different and independently transformed parents from the A8-1 and A8-5 families and which contain six and five copies of *Ds-bar*, respectively, we identified in the F₂ generation five TNP lines from each family. Figure 1 shows a DNA-blot hybridization of samples from different F₂ lines derived from A18-5. In this blot the hybridization pattern of DNA from three plants containing a single copy of *Ds-bar* is seen as different-sized *Hind*III fragments. Each of the *Hind*III sites is unique and is predicted to be in the genomic DNA flanking the site of *Ds-bar* integration. The pres-

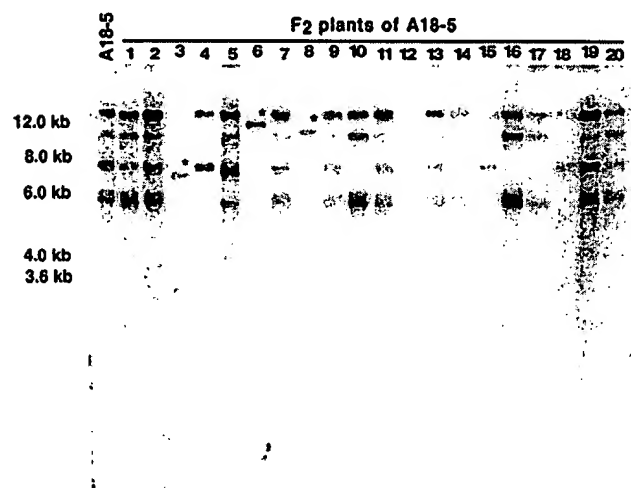


Figure 1. Transposon-mediated generation of single-copy transgenic plants. DNA-blot hybridization shows the integration pattern of *Ds-bar* after *Hind*III digest of genomic DNA from F₁ parent, A18-5 (far left lane), and 20 of its F₂ progeny. In three plants (i.e. nos. 3, 6, and 8), a single *Ds-bar* cassette has transposed to an unlinked site, segregating away from other copies. The asterisk above the band marks the position in single-copy *Ds-bar* plants that differs from the parental bands. *M*, markers in kilobases are indicated on the left.

ence or absence of *AcTPase* was, in all cases, analyzed by PCR using *AcTPase*-specific primers (data not shown). Other single-copy events were analyzed in an identical manner (data not shown).

Transgene and Transgene Expression Stability

The physical transmission of *bar* from the single-copy TNP lines followed Mendelian segregation in the F₃ generation in the newly created single-copy, *Ds-bar* plants, as evidenced by DNA-blot hybridization analysis of genomic DNA. In the TNP and nTNP lines from families A8-1, A8-5, A1-5, and A18-5, functional expression of the *bar* gene product was analyzed in later generations by monitoring herbicide resistance. While screening the F₂ populations from the four families to identify single-copy *Ds-bar* individuals, plants were painted with Basta. All TNP lines in the F₂ generation were completely resistant to the herbicide. In contrast, up to 40% of all nTNP lines derived from the four families showed reduced numbers of Basta-resistant plants, consistent with transgene silencing.

Transgene-expression stability of lines derived from the four families was monitored in advanced generations in 17 nTNP lines and 35 TNP lines, all of which were Basta-resistant in the F₂ generation. Between 40 and 50 F₃ and F₄ plants, derived from each of the 52 F₂ lines, were tested for herbicide sensitivity. To avoid damage or death of the entire plant in the case of herbicide sensitivity and to ensure seed set, only one leaf of each plant was painted with Basta. We observed no expression of the *bar* gene product in F₃ progeny of 14 of the 17 nTNP lines (82.4%), as evidenced by sensitivity of the plants in the line to Basta (Table I). In the F₃ generation 100% of all nTNP lines derived from multicopy families A1-5 and A18-5 contained plants in which Basta sensitivity was evident. In contrast, only six of the 35 TNP lines (17.1%) produced F₃ progeny showing transgene silencing (Table I). The number of plants within nTNP lines that showed evidence of transgene silencing was significantly higher statistically ($P < 0.1\%$; chi-square analysis) than within TNP lines (Table I). Even though only seeds from Basta-resistant F₃ plants were collected, transgene silencing continued to persist into the F₄ generation. Only one of 17 nTNP lines produced completely resistant F₄ plants; 94% of

all nTNP lines contained between 1% and 48% of plants with silencing of the *bar* gene product (Table I; Fig. 2). It is striking that all 29 TNP lines, which were completely Basta-resistant in F₃, also produced completely resistant F₄ plants. Among F₄ progeny from the six TNP lines that exhibited transgene silencing in the F₃ generation, plants were again Basta-sensitive in numbers comparable with those in the nTNP lines (data not shown). Progeny of one TNP plant line (A1-5-54) derived from family A1-5 were completely Basta-resistant in the F₃ generation, but showed signs of transgene expression instability in F₄.

Analysis of the Integration Sites of *Ds-bar*

To analyze the redundancy of the genomic region into which the *Ds-bar* element from single-copy nTNP and TNP plants had inserted, DNA blots of *Hind*III-digested DNA from non-transgenic barley plants (var Golden Promise) were hybridized with probes from genomic regions flanking the *Ds* element. Flanking regions were isolated from the single-copy nTNP plant (A8-1-5), three silenced TNP plants (e.g. see Fig. 3, A8-1-51), and six stably expressing TNP plants (e.g. see Fig. 3, A8-1-22, -34, -85, and -120) that have *Ds-bar* in different locations. Analysis of the DNA blots showed that the single-copy *Ds-bar* element from the silenced nTNP plant A8-1-5 had integrated into a highly repetitive genomic region. Two of the three TNP plants with silenced transgene expression (e.g. see Fig. 3, A8-1-51) had transposed into highly or moderately repetitive regions of the barley genome. The *Ds-bar* elements from all stably expressing TNP plants had transposed to single-copy or low-copy regions (up to three hybridizing fragments) of the barley genome (e.g. Fig. 3, A8-1-22, -34, -85, and -120 and data not shown). Only one line, A8-1-25, in which *Ds-bar* had inserted into a non-repetitive genomic region (data not shown), exhibited signs of transgene silencing and the silencing was observed in only one of 31 (3%) *bar*-containing F₄ plants.

Methylation Analysis of the Promoter and Coding Region of *Ds-bar*

To assess the methylation status of the *Ds-bar* element a series of DNA hybridization blots were con-

Table I. Transgene expression stability in nTNP and TNP plant lines

F ₁ Plant	No. of Copies	No. of Lines with Transgene Expression Instability/Total Lines Analyzed					
		F ₂		F ₃		F ₄	
		nTNP ^a	TNP ^b	nTNP	TNP	nTNP	TNP
A8-1	1	6/8 (75%)	0/15 (0%)	6/8 (75%)	2/15 (13%)	7/8 (88%)	2/15 (13%)
A8-5	1	4/5 (80%)	0/10 (0%)	4/5 (90%)	2/10 (20%)	5/5 (100%)	2/10 (20%)
A1-5	6	N.D.	N.D.	2/2 (100%)	1/5 (20%)	2/2 (100%)	2/5 (40%)
A18-5	5	N.D.	N.D.	2/2 (100%)	1/5 (20%)	2/2 (100%)	1/5 (20%)

^a nTNP lines are "non-transposed," containing *Ds-bar* at the original integration site and do not contain *AcTPase*. ^b TNP lines are "transposed" and are progeny of F₁ plants selected for a single copy of *Ds-bar* transposed to a new location.

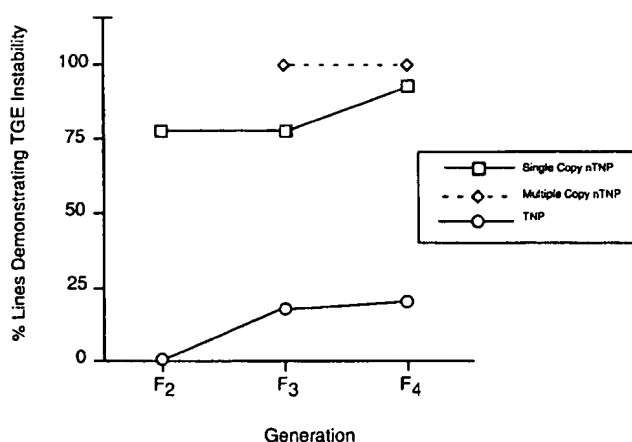


Figure 2. Average frequency of transgene expression instability in F₂, F₃, and F₄ populations. Lines from F₂, F₃, and F₄ populations were assessed for functional expression of the product of *bar* by testing for Basta sensitivity. Percentages represent the number of lines in which at least one plant exhibited Basta sensitivity divided by the total number of lines per family tested. TNP, Transposed *Ds-bar* element, no *ActPase*; nTNP, *Ds-bar* element remaining at original site of integration following bombardment, no *ActPase*; TGE, transgene expression.

structured to analyze the *ubiquitin* promoter region driving *bar* gene expression and the *bar*-coding region itself. DNAs from different silenced and non-silenced nTNP and TNP plants were digested with six different methylation-sensitive enzymes, and hybridization patterns with multiple probes were analyzed to provide information about the methylation status at specific restriction sites. The data in Figure 4A shows the results of digestion with *Hpa*II; the positions of restriction sites located within the *ubiquitin* promoter and first intron region are indicated in Figure 4B. All DNA samples from Basta-sensitive plants showed evidence of methylation at certain *Hpa*II sites in the *ubiquitin* promoter region. In contrast, DNA samples from Basta-resistant plants showed no evidence of methylation at these *Hpa*II sites. Based on the map position of *Hpa*II sites (Fig. 4B) and predicted fragment sizes after *Hpa*II digestion, it appears that certain sites are more prone to becoming methylated than are others. For example, *Hpa*II sites I and III were non-methylated in all plants shown in Figure 4A, resulting in fragment sizes of 850 or 1,150 bp after hybridization with probe A (Fig. 4B). Analysis of additional plants, however, showed that in a few cases *Hpa*II sites I and III were hypermethylated (data not shown). In contrast to that situation, *Hpa*II sites II and V were always methylated in silenced plants, as confirmed by hybridization with probes B and C (data not shown).

Restriction digests with other methylation-sensitive enzymes showed an increased level of methylation in the promoter region in all silenced plants (data not shown). The methylation pattern within the analyzed promoter/intron region varied

from plant to plant, but, in general, was higher in Basta-sensitive F₄ plants than in F₃ plants. Figure 4B shows a diagram of the analyzed promoter/intron region with the sites indicated that were found to be methylated in at least some plants. In most silenced plants only a few of the sites shown in Figure 4B were methylated or partially methylated; however, in non-silenced plants none of these sites were methylated. The highest degree of methylation was found in silenced single-copy nTNP plants and in silenced TNP plants in which the transposed *Ds-bar* element had reinserted into highly repetitive genomic regions (e.g. Fig. 3, plant A8-1-51).

DNase I Sensitivity Tests

To determine if the silencing observed in nTNP and TNP plants is correlated with changes in the contiguous chromatin structure, the DNase I sensitivity of the transgene region was determined using isolated nuclei from several silenced and non-silenced plants.

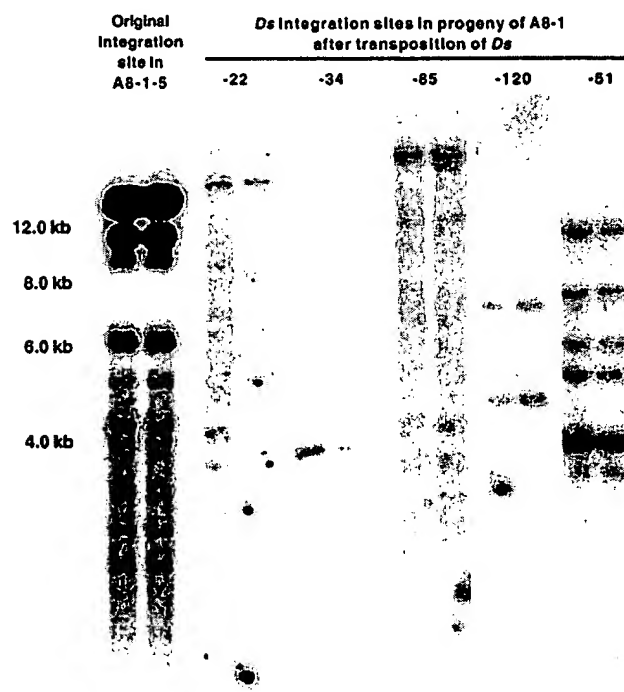


Figure 3. Analysis of *Ds-bar* integration sites. Genomic DNA flanking single-copy *Ds-bar* elements was isolated from six different transgenic plants by thermal asymmetric interlaced-PCR. PCR fragments were then used as hybridization probes with DNA blots of *Hind*III-digested genomic DNA from non-transgenic plants. The two lanes on left are results after hybridization with a probe specific to the genomic DNA flanking the original *Ds-bar* insertion site of line A8-1-5. Other sets of lanes show results after hybridization with probes flanking the insertion sites from five lines in which *Ds-bar* has transposed to a new location: four lines that stably express the transgene, e.g. nos. 22, 34, 85, 120, and one line that does not, 51. M, markers in kilobases are indicated on left.

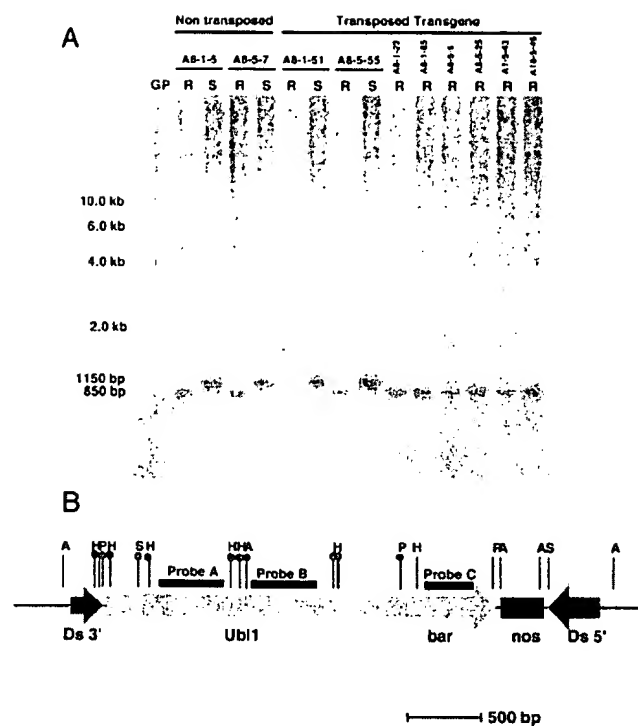


Figure 4. A, Methylation analysis of Basta-sensitive and Basta-resistant plants from lines with transposed and non-transposed *Ds-bar* cassette. DNA blots of *HpaII*-digested genomic DNA from Basta-sensitive and Basta-resistant plants were hybridized with probe A (B) from the 5' end of the ubiquitin promoter of the *Ds-bar* cassette. Lanes containing DNA from Basta-resistant plants have an 850-bp hybridization fragment, as expected for a non-methylated *HpaII* site in the *ubiquitin* promoter region. Digests of DNA from Basta-sensitive plants have fragments of 1,150 bp, indicating methylation of an *HpaII* site in the immediate 5' region of probe A (B). R, Basta-resistant; S, Basta-sensitive; GP, Golden Promise non-transgenic control. B, Methylation analysis of promoter and coding region of *Ds-bar* cassette in Basta-sensitive lines. Diagram summarizes results of digests with different methylation-sensitive enzymes (A, *AvaI*; H, *HpaII/MspI*; P, *PstI*; Sc, *SacII*; and S1, *SalI*) and hybridization with three different probes (A, B, and C). *HpaII/MspI* sites are numbered I through VII from left to right. A total of 20 different Basta-sensitive plants from eight different lines were analyzed. Based on the size of hybridization fragments and information regarding the restriction sites in the *Ds-bar* cassette, the position of specific methylated sites was determined. In some cases different *HpaII/MspI* sites are not sufficiently separated to allow differentiation between individual sites. In accordance with this, closely connected sites were marked as methylated if at least one of the sites was methylated. A circle on top of the lines symbolizes methylation was detected at that site in at least some plants. Size bar indicates 500 bp.

Chromatin of two silenced nTNP plants, four silenced TNP plants, and five non-silenced plants was analyzed. Figure 5 shows the results of a representative experiment. The hybridization signal of the expected 1.9-kb fragment in nTNP plant A8-1-5, which shows unstable expression and has a single *Ds-bar* element, decreases slowly over a 20-min period, indicative of low accessibility of the transgene region to DNase I. In contrast, in TNP line A8-1-85, which

exhibits stable expression of the transgene, the hybridization signal decreases rapidly and disappears completely after a 15-min incubation period with DNase I. The transgene of a silenced TNP plant (A8-1-51) exhibited a similar low accessibility to DNase I as that observed in silenced nTNP plants. Analysis of the comparison of the DNase I sensitivity of different silenced and non-silenced TNP plants showed that silencing was associated with a compact chromatin structure in the vicinity of the transgene in 10 of 11 analyzed plants. The chromatin of one silenced TNP plant showed a DNase I sensitivity that was comparable with the sensitivity of chromatin in non-silenced TNP plants. The accessibility to DNase I varied between different non-silenced TNP lines, but was very similar between individual plants from the same TNP line (data not shown).

DISCUSSION

Transgene expression instability is a common phenomenon in genetically transformed plants from monocot species (Iyer et al., 2000). The majority of cases of transgene silencing can be correlated with the existence of multicopy inserts, sequence rearrangements, and the random nature of integration into the genome, all of which occur frequently when methods of direct gene transfer are used for transfor-

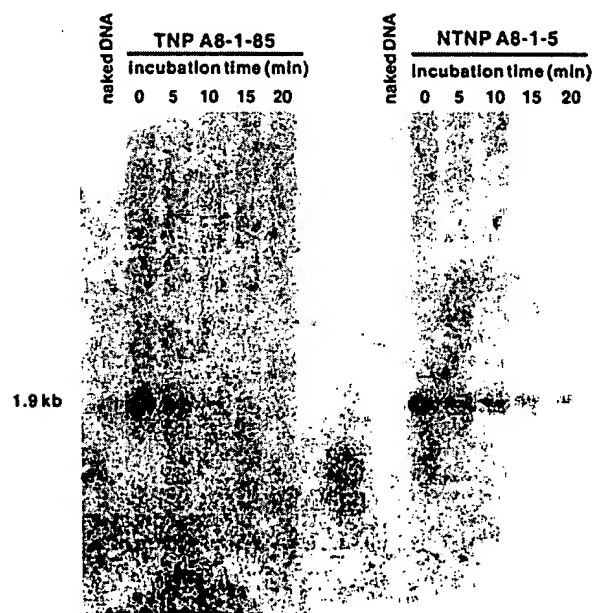


Figure 5. Analysis of chromatin structure near *Ds-bar* cassettes from lines with a transposed or non-transposed *Ds-bar* cassette. Intact nuclei from plants with (i.e. TNP A8-1-85) or without (i.e. nTNP A8-1-5) transposed *Ds-bar* were treated with DNase I for 0 to 20 min. DNA was isolated, digested with *BglI* to obtain fragments of a specific reference size (1.9 kb), electrophoretically separated, blotted, and hybridized with probe C (Fig. 4B). Naked DNA (no intact chromatin) from both plants, treated for 2 min with DNase I, served as a control.

mation (Hiei et al., 1994). Transgene silencing occurs in single-copy transgenic plants due to other factors such as insertion position, but the silencing is much less frequent than in multicopy plants. With most present methods of transformation, it is often necessary to screen large numbers of independent transformants to identify single-copy transgenic plants. This makes the process labor intensive, expensive, and, in recalcitrant species, essentially not feasible. These facts make the development of a single-copy gene delivery system that inserts genes into transcriptionally active regions of potential value.

Agrobacterium-mediated gene delivery in cereals leads to lower copy-number insertions, and single-copy transgenic plants are more frequent (Cheng et al., 1997; Tingay et al., 1997). This method, however, does not eliminate the problem of gene silencing in cereals (Ishida et al., 1996; Park et al., 1996) because even *Agrobacterium*-generated transgenic plants containing a single-copy of the transgene showed evidence of silencing (Waterhouse et al., 1998).

In the present study we describe a different method of generating large numbers of single-copy transgenic plants in barley by crossing *AcTPase*-expressing plants with plants containing one or multiple *Ds*-elements into which an herbicide resistance gene was inserted. We show that a single *Ds-bar* element can transpose from a multicopy locus to linked and unlinked sites. In the latter case the element can segregate away from the other copies of the *Ds* element and from the *AcTPase* gene (Koprek et al., 2000), physically stabilizing the element in its new location. The resulting single-copy element can be re-activated by providing *AcTPase* in *trans*. In this way, hundreds of independent, single-copy transgenic plants can readily be generated and the transgene of interest can be separated away from the rest of the vector sequences, e.g. plasmid backbone and selectable marker genes.

Analysis of transgene expression in plants carrying *bar* in new locations following transposition showed that plants from most TNP lines were completely Basta-resistant in the F_3 and F_4 generation, exhibiting no signs of necrosis after herbicide treatment. In contrast, a large proportion of lines with one or multiple copies in their original integration site (82% in F_3 and 94% in F_4) showed signs of transgene inactivation. This striking difference occurred in the F_4 generation despite the fact that only Basta-resistant F_3 plants were chosen for generation-advance. In all cases studied, gene-silenced plants exhibited increased methylation of cytosine residues in the *ubiquitin* promoter region linked to *bar* and a more condensed chromatin structure in the immediate vicinity of the transgene or the transposed silenced *Ds-bar* element. These observations are consistent with the observations of others that transcriptional gene silencing often correlates with changes in the methylation status (Stam et al., 1997a, 1997b) and with a locally con-

densed chromatin structure (Ye and Signer, 1996; van Blokland et al., 1997).

Despite the dramatic improvement in transgene expression stability in the TNP plants, silencing was observed in a few TNP lines in our experiments, indicating that additional factors play a role in transgene expression stability. The *Ds-bar* construct contains short, inverted repeats and inverted repeats are known to induce transcriptional and post-transcriptional gene silencing (for review, see Muskens et al., 2000). In addition, methylation-induced, heritable, and reversible transposon inactivation has been described for all major maize transposons (Fedoroff and Chandler, 1994). This phenomenon can be triggered by the terminal inverted repeats of the transposon, as well as by the transposon copy number. Although copy number is not a factor, the inverted repeats are present on the cassette. This mechanism could account for some of the silencing in TNP and nTNP lines in our experiments. However, since all TNP plants, whether silenced or not, contain the same terminal inverted repeats and subterminal repeats of *Ds* and in the same structural context in the single intact *Ds* copy, this would not seem to explain the differences in expression stability among plants from the same line. The analysis of transgene expression in advanced generations will show if the *Ds-bar* elements go through cycles of silencing that are typical for maize transposable elements. To date, tracking transgene expression stability through the F_6 generation in numerous lines has turned up little evidence of transgene expression instability (T. Koprek and S. Rangel, unpublished data).

Another factor that might play a decisive role in transgene expression stability is the nature of the chromosomal location of the transgene insertion, which cannot be controlled and varies from line to line. In our experiments most transposed *Ds-bar* elements tested (80%) re-inserted into single-copy genomic DNA regions and all but one of these lines produced stably expressing progeny. The existence of the one unstable single-copy line indicates that apart from insertion into genomic DNA of low redundancy, other factors like vicinity to matrix attachment regions (Spiker and Thompson, 1996; Holmes-Davis and Comai, 1998), isochore compatibility of the transgene with the flanking genomic DNA (Kumpatla et al., 1998; Matzke and Matzke, 1998), and higher-order chromatin structure (Sun and Elgin, 1999) might influence transgene expression, but these other factors do not appear to affect transgene expression stability in many *Ds*-delivered lines.

Analysis of chromosomal DNA from TNP lines A8-1-51 (Fig. 3) and A8-5-55 (data not shown) in which *Ds-bar* reinserted into repetitive DNA sequences showed a high degree of methylation in the *ubiquitin* promoter region of the transgene (Fig. 4, A and B) and plants derived from these lines showed

signs of transgene silencing. Insertion of transgenes in or near repetitive DNA or heterochromatic regions has been shown to correlate with inactivation of the transgene (Pröls and Meyer, 1992). The results of gene-tagging experiments with *Ac/Ds* in *Arabidopsis* and tomato show that *Ds* elements frequently transpose into transcriptionally active regions (Pari-nov et al., 1999; Meissner et al., 2000), and this predisposition could be an explanation for the high percentage of TNP plants that express *bar* stably over several generations.

Our results show that the use of transposable elements as a transporter for transgenes leads to the generation of large numbers of independent single-copy transgenic plants from only two original transfor-mants, one with *Ds* and one with transposase—a situation that has positive implications for recalcitrant species and varieties within a species. In addition, the increased stability of transgene expression in most TNP plants, as well as the ability to eliminate selectable marker genes and other vector sequences, gives rise to a system of gene delivery that has great utility for generating crop plants with improved ag-ronomic characteristics. The system described here can also be used as a valuable tool to gain further insight into mechanisms of gene silencing.

MATERIALS AND METHODS

Plasmids

Plasmid pSP-Ds-Ubi-*bar* containing the *Ds-bar* element consists of the *Streptomyces hygroscopicus* phosphinothricin acetyl transferase gene (*bar*) under control of the *Ubi1* promoter and first intron from maize and the *nos* terminator as a 0.9-kbp *Clal-NotI* restriction fragment. The *Ubi1-bar-nos* cassette is flanked by a 254-bp 5' sequence and a 340-bp 3' sequence from *Ds*, derived from pDs7 (Wirtz et al., 1997) as a 0.59-kbp *Sall-BamHI* restriction fragment. The construction of the entire plasmid has been described in detail previously (McElroy et al., 1997; Koprek et al., 2000).

Plant Material

Transgenic barley (*Hordeum vulgare* var Golden Promise) plants containing the *Ds* element with a *ubiquitin-bar* ex-pression cassette as an insert or the *AcTPase* gene under transcriptional control of the *ubiquitin* promoter from maize or the putative *AcTPase* promoter region were gen-erated by particle bombardment of immature embryos (Wan and Lemaux, 1994). *AcTPase*-expressing plants were crossed with plants that contained one, five, or six *Ds-bar* copies. Resulting F₁ plants were self-pollinated; F₂ plants in which *Ds* had transposed to an unlinked site and segre-gated away from linked sequences were identified by DNA-blot hybridization and PCR analysis (Koprek et al., 2000).

Transgene Expression Test

Plants negative for the *AcTPase* gene and containing single or multiple *Ds-bar* copies in their original integration site (non-transposed, nTNP) or a single transposed *Ds-bar* in a new location (transposed, TNP) were treated with the herbicide Basta to monitor expression of *bar* (Wan and Lemaux, 1994). A total of 17 nTNP lines (eight lines derived from A8-1, five lines from A8-5, and two lines each from A1-5 and A18-5) and 35 TNP lines (15 lines derived from A8-1, 10 lines from A8-5, and five lines each from A1-5 and A18-5) were tested. When plants were in the three-leaf stage, 2.5 cm-long leaf segments were painted with an aqueous solution containing 0.5% (v/v) Basta and 0.1% (v/v) Triton X-100 using a cotton swap. Plants showing any sign of necrosis due to the herbicide were scored as sensitive. In F₃ generation, plants with a transposed *Ds-bar* cassette were expected to segregate the *Ds-bar* element in a 3:1 ratio. Any plants scored as sensitive were analyzed by PCR to confirm the presence or absence of the transgene; sensitive plants containing the transgene were scored as silenced. Resistant plants were self-pollinated and progeny of these plants (F₄ generation) were analyzed in an identi-cal manner.

DNA-Blot Hybridization

Genomic DNA was isolated from leaf tissue (Cone, 1989) when plants were in the four-leaf stage. To identify plants containing a single copy of *Ds-bar*, 10 µg of DNA was digested with *HindIII*, which does not cut within the 3.6-kb *Ds-bar* fragment. The digested DNA was separated in 0.8% (w/v) agarose gels, transferred to nylon membranes (Bio-Rad, Hercules, CA), and hybridized with radioactively la-beled (Promega, Madison, WI) *Ds*-specific probe. Analysis of the methylation status of *bar* and the mapping of its location in non-silenced and silenced plants was per-formed. Genomic DNA was digested to completion with *AvaI*, *HpaII*, *MspI*, *PstI*, *SacII*, and *Sall* (*HpaII* was purchased from New England Biolabs, Beverly, MA), all other en-zymes were from Promega) alone or in combination with the non-methylation sensitive enzymes *DraI* or *BglI*. Di-gested DNA was treated as above. Hybridizations were carried out consecutively with *bar* expression cassette probes A, B, and C (Fig. 4B). Blots were stripped after exposure to x-ray film and were re-probed according to manufacturer's instructions.

PCR Analysis

Genomic DNA (0.5 µg) was subjected to PCR amplifica-tion in a thermocycler (model PTC-100, MJ Research, Waltham, MA). PCR reactions (50 µL) contained 1× PCR buffer (Promega), 200 µM of each dNTP, 1.5 mM MgCl₂, 1 µM primer, 1% (w/v) dimethyl sulfoxide, and 2.5 units of *Taq* DNA polymerase (Promega). The primer pairs used for the *bar*-coding region were BAR5': (5'-TGC ACC ATC GTC AAC CAC TA-3') and BAR3': (5'-ACA GCG ACC ACG CTC TTG AA-3') and were used to produce a PCR product of 311 bp. PCR reactions were performed with an initial

denaturation step at 94°C for 2 min followed by 10 cycles of a touch-down program with decreasing annealing temperatures from 65°C to 60°C in increments of -0.5°C per cycle for 30 s, an extension at 72°C for 30 s, a denaturation at 94°C for 45 s, a subsequent 25 amplification cycles for 30 s at 60°C, 30 s at 72°C, and 45 s at 94°C, and a final extension at 72°C for 5 min. PCR products were analyzed by gel electrophoresis in 1.1% (w/v) agarose gels.

Isolation and Analysis of Regions Flanking Ds Inserts

The redundancy of the DNA flanking the integration site of transposed and non-transposed *Ds*-elements was analyzed by hybridizing DNA blots of *Hind*III-digested genomic DNA from non-transgenic var Golden Promise plants with isolated *Ds*-flanking genomic DNA regions. Genomic DNA flanking *Ds*-element inserts from 10 different transposition events was isolated using thermal asymmetric interlaced-PCR (Liu et al., 1995) with random primers as described previously (Koprek et al., 2000). Specific amplified tertiary PCR products were analyzed on 1.5% (w/v) agarose gels, isolated using the QIAquick gel extraction kit (Qiagen, Valencia, CA), and used as probes for DNA-blot hybridizations as described above.

Nuclei Isolation and DNase I Sensitivity Test

Five grams of young leaves were ground in liquid N₂; the powder was resuspended in 25 mL of Hamilton buffer (10 mM Tris-HCl, pH 7.6, 1.14 M Suc, 5 mM MgCl₂, and 5 mM β-mercaptoethanol; Hamilton et al., 1972) and the slurry was gently stirred and filtered through three layers of Miracloth (Calbiochem, La Jolla, CA) in 10 mL of the same buffer. The final pellet was resuspended, washed in 5 mL of DNase I digestion buffer (50 mM Tris-HCl, pH 8.0, 0.3 M Suc, 5 mM MgCl₂, 1.5 mM NaCl, 0.1 mM CaCl₂, and 5 mM β-mercaptoethanol), and centrifuged at 1,000g for 10 min. The pellet was resuspended in 1,550 μL of DNase I digestion buffer and 50 μL of the nuclei suspension was stained with 4',6-diamino-phenylindole. Nuclei were counted under a fluorescence microscope. All manipulations were carried out at 4°C.

For DNase I digestion, aliquots containing 5 × 10⁵ nuclei (usually in 100–150 μL) were transferred into separate reaction tubes and DNase I digestion buffer was added to a final volume of 200 μL per reaction. Nuclei were treated with 1 unit/mL DNase I (Promega) at 25°C for 0, 5, 10, 15, and 20 min. The reaction was stopped by adding 40 μL of stop buffer (0.25 M EGTA, 0.25 M EDTA). Chromatin-free (naked) DNA was separated from the isolated nuclei and treated with 1 unit of DNase I for 2 min. DNA was extracted and purified as described above, resuspended in 20 μL of Tris-EDTA, and digested with *Bgl*I to create reference-sized DNA fragments. The DNA was separated on 0.8% (w/v) agarose gels, blotted, and hybridized as described above with a probe specific for the *bar*-coding region (probe C; Fig. 4B).

Received December 8, 2000; returned for revision December 17, 2000; accepted December 20, 2000.

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